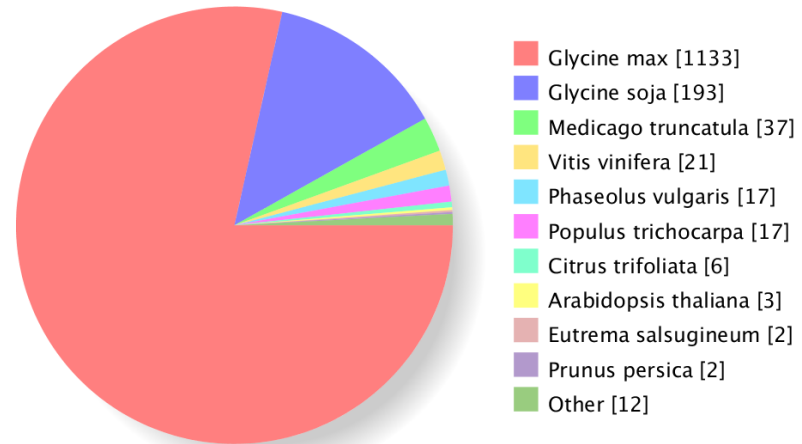


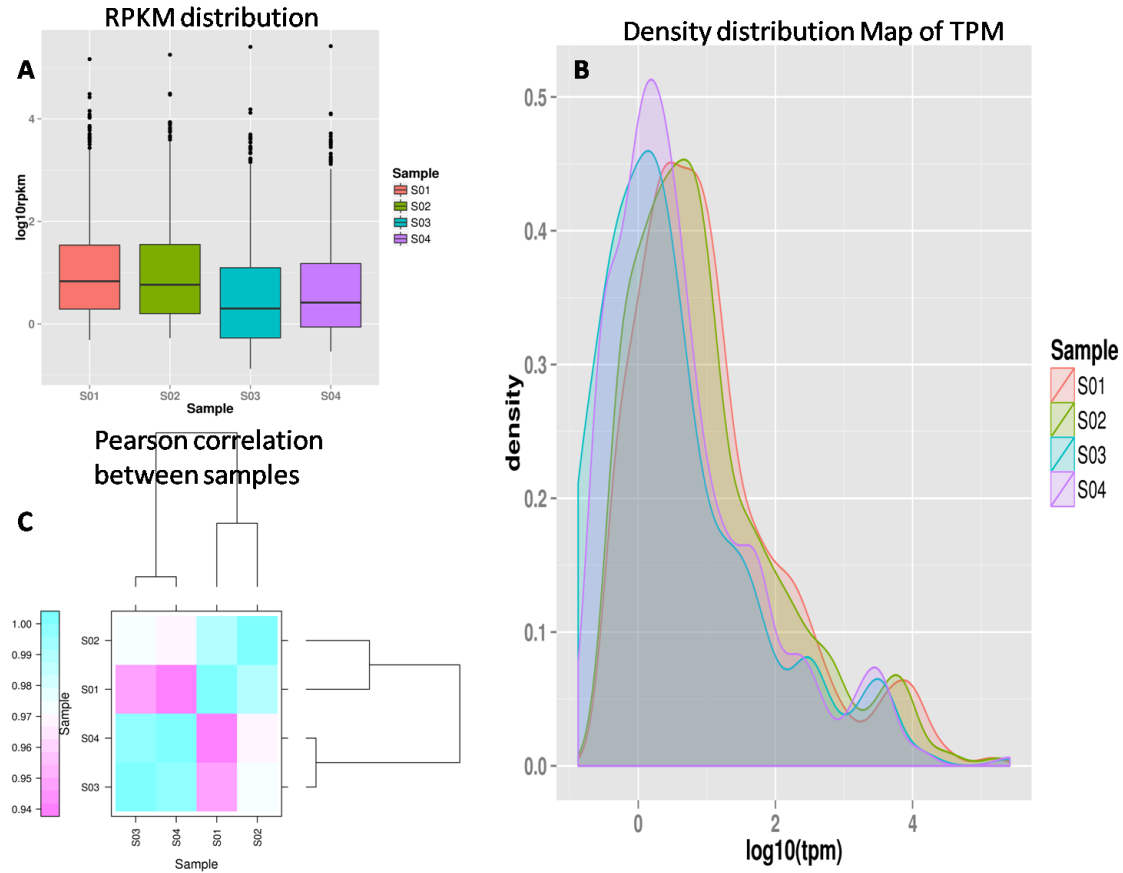
Supplementary Figure 1 sRNA flowchart of sequencing information analysis

Nr Homologous Species Distribution



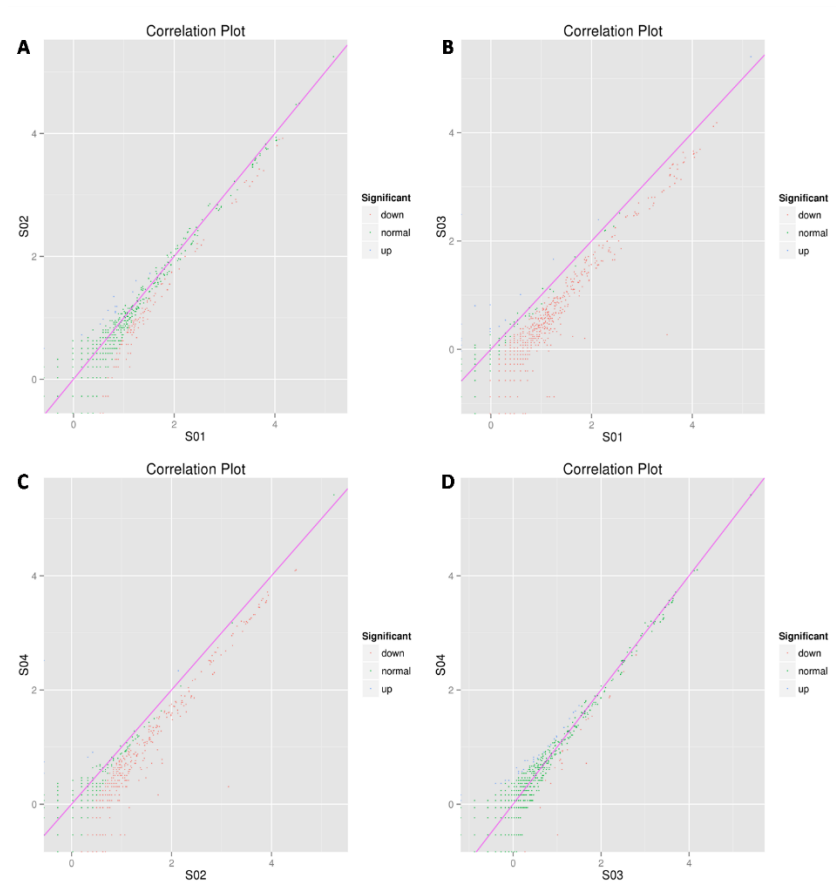
Supplementary Figure 21 Homologues species of miRNA families found in different plants

Note: The colors represent the accumulation of homologues.



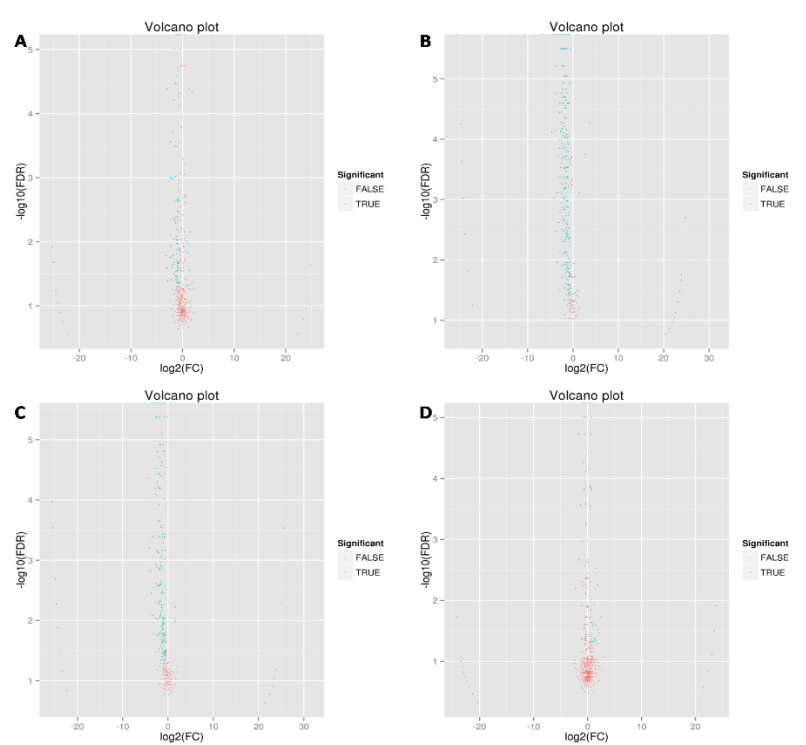
Supplementary Figure 3 RPKM and TPM distribution of 4 libraries along with their Pearson correlation

Note: The curves of different colors represent different samples, the horizontal axis of the points on the curve indicates the number of the corresponding sample TPM, and the ordinate of the points indicates the probability density. It can be seen from the above diagram that the miRNA expression of the samples is consistent with high consistency.



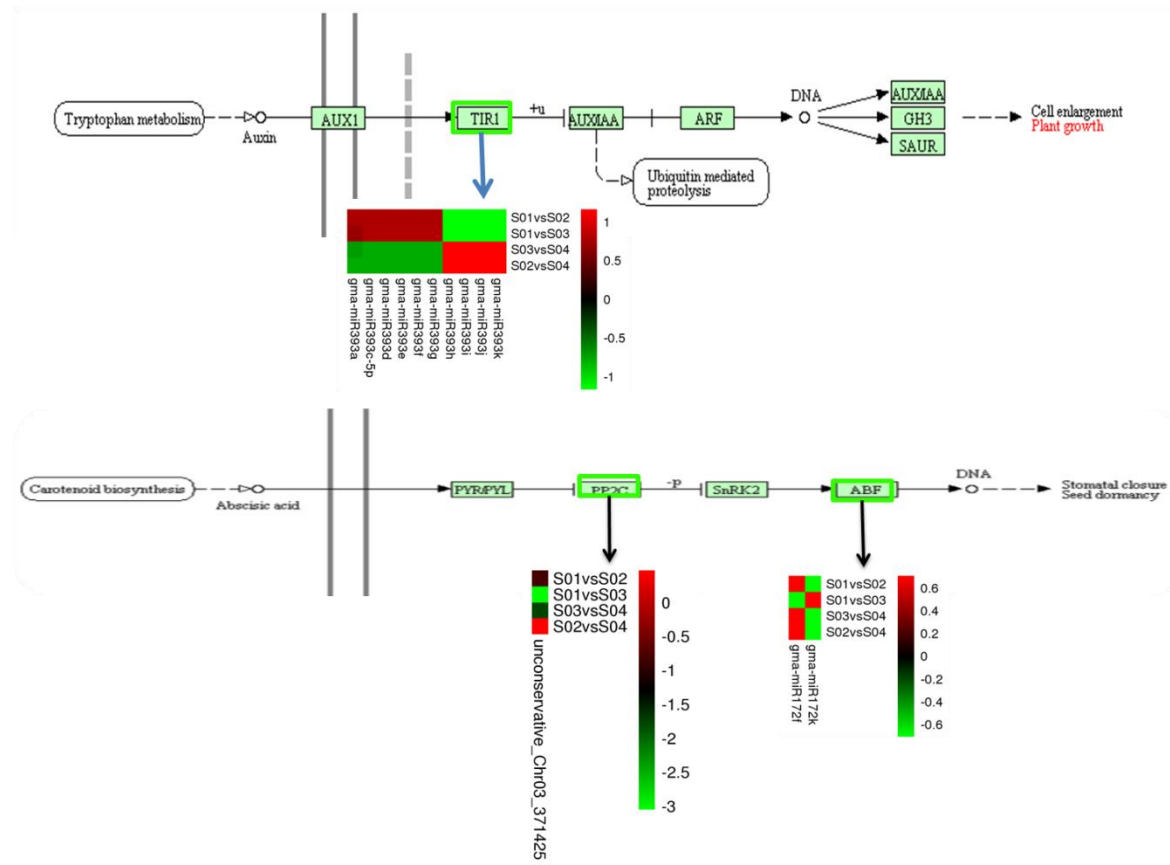
Supplementary Figure 4 Correlation plot between the different samples

Note: The red dot means that the miRNA is down-regulated; the green dot means that the expression is normalized; the blue dot means up-regulated miRNA. A: S01vsS02, B: S01vsS03 C: S02vsS04 D: S03vsS04

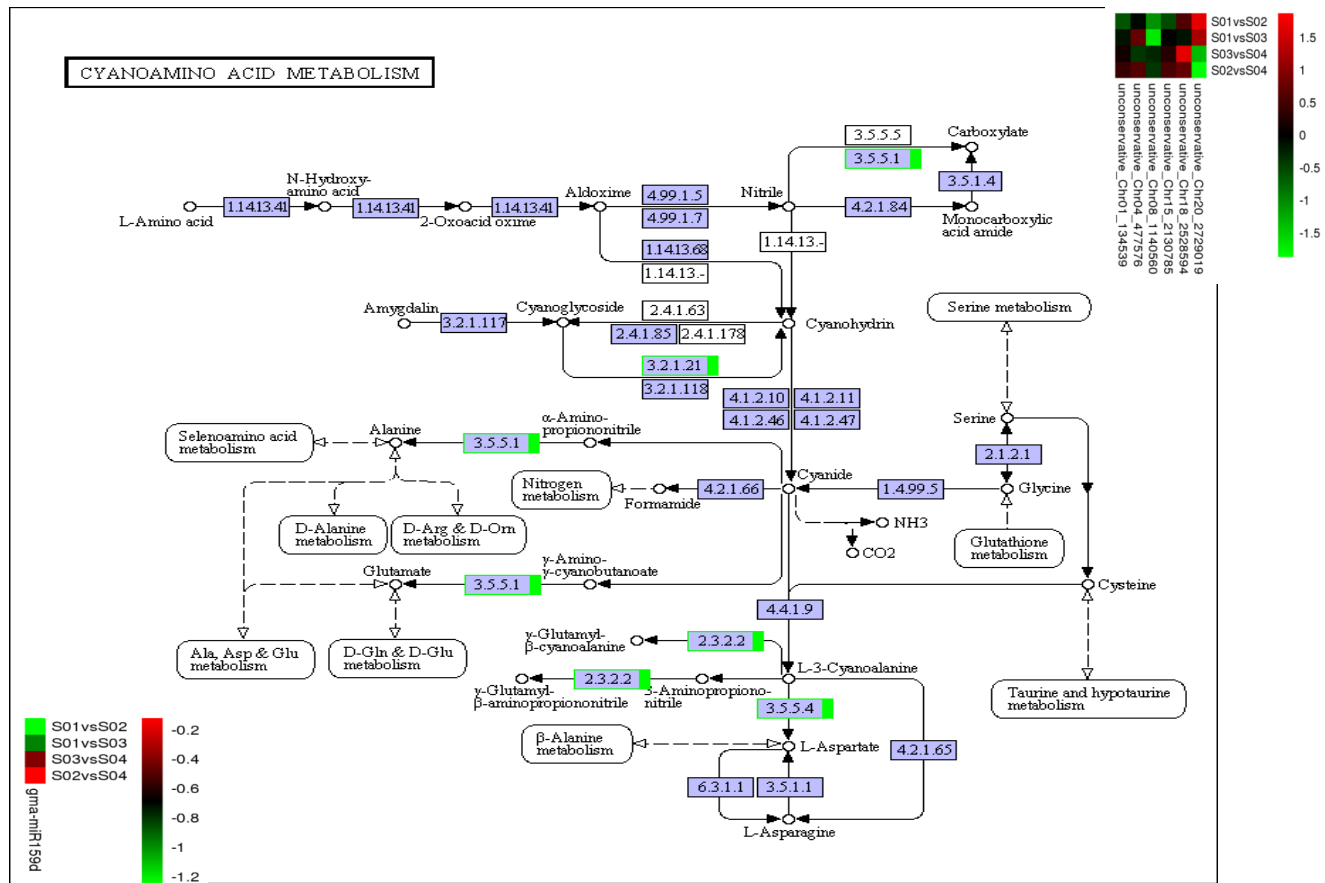


Supplementary Figure 5 The difference expression miRNA volcano map

Note: Each point in the volcanic map of the differential expression represents a miRNA, and the horizontal axis represents the value of the difference in the expression of a miRNA in two samples; the ordinate represents the negative pair value of the error discovery rate. The greater the absolute value of the coordinate axis, the greater the difference of expression amount between two samples, the greater the ordinate values, the more obvious the difference expression, the more accurate the difference expression miRNA. The blue dots in the Fig represent the differential expression miRNA, and the red dots represent the miRNA of the differential expression. **A:** S01-Nannong10-1 mock, **B:** S02-Nannong10-1 12hpi, **C:** S03-06-070583 mock, **D:** S04-06-070583 12hpi

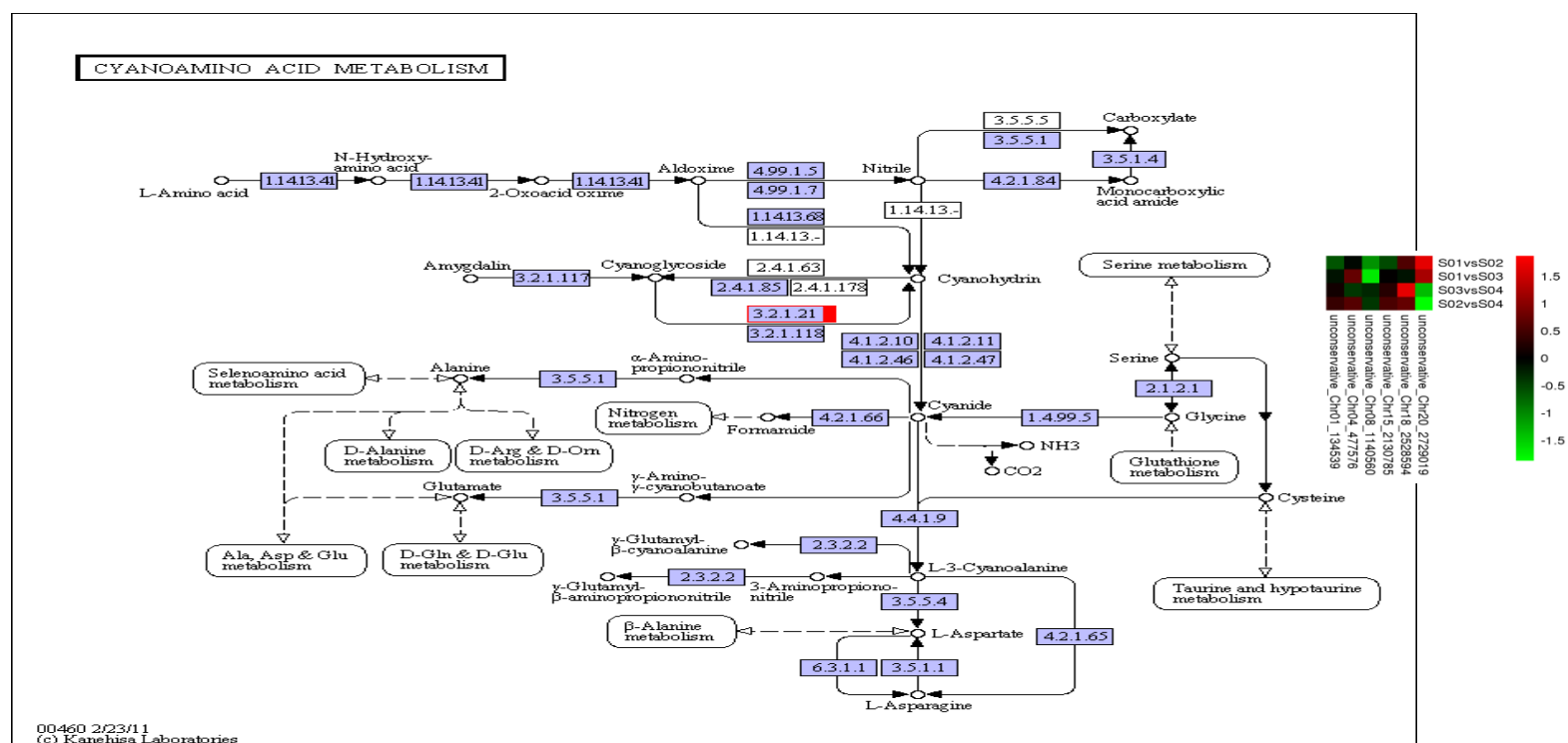


Supplementary Figure 6a-b Plant-hormone signaling pathway in S01vs S02 along with their DEGs

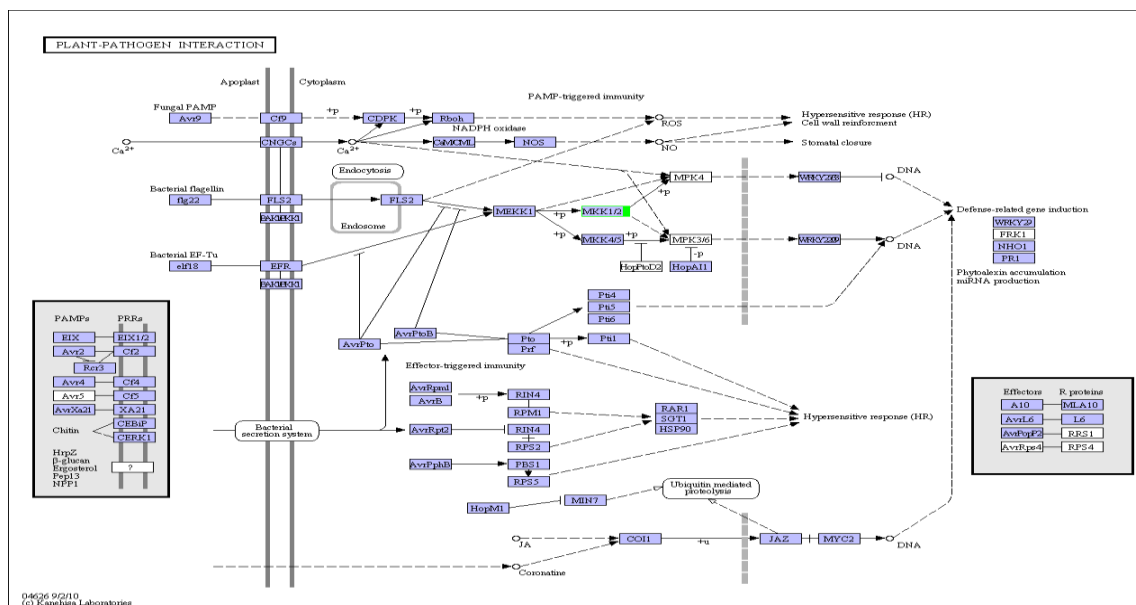


Supplementary Figure 7a Cyanoamino acid metabolism showing the down-regulated DEGs in S01 vs S02

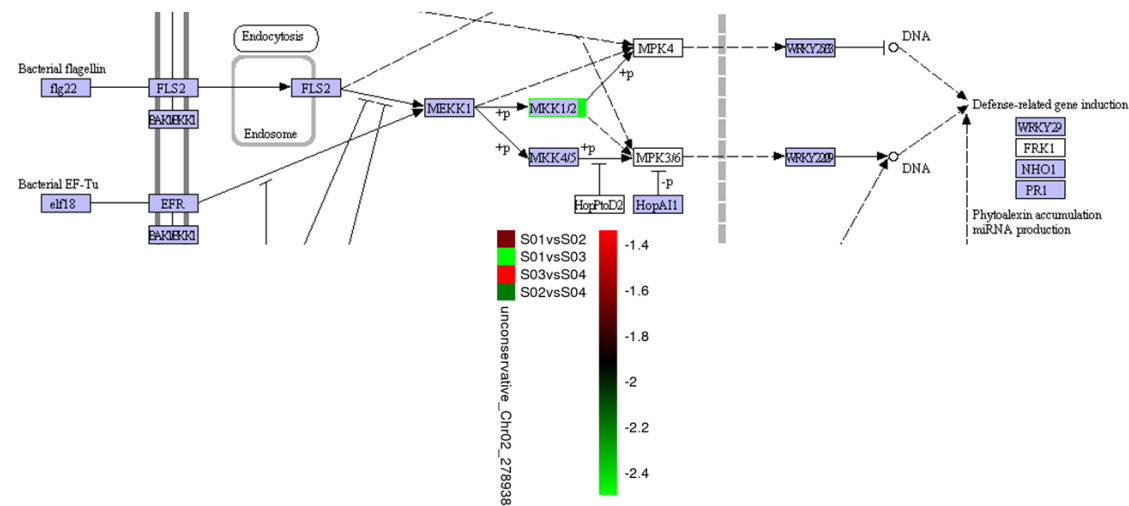
Note: At the top right corner and bottom left corner of the picture the novel and known miRNAs are represented with a heat map of all four possible combinations along with their expression.



Supplementary Figure 7b Cyanoamino acid metabolism showing the up-regulated DEGs in S03 vs S04



Supplementary Figure 9a Plant pathogen interaction pathway in S01 vs S02



Supplementary Figure 9b Plant pathogen interaction pathway S03 vs S04

Note: Compared with the control group, the red box-labeled enzymes are related to the up-regulated genes, and the green-box-labeled enzymes are related to the reduced genes. The numbers in the box represent the number of enzymes (EC numbers), and the entire pathway is composed of complex biochemical reactions catalyzed by enzymes, which are labeled with differentially expressed miRNA target genes, depending on the differences between the subjects.